WHAT IS CLAIMED IS:

1. A method of classifying or typing a prokaryote to a class or a type, the method comprising the step of characterizing at least one polymorphic simple sequence repeat locus in a genome of said prokaryote and, based on a characterization of said polymorphic simple sequence repeat, classifying or typing said prokaryote to a class or a type.

2. The method of claim 1, wherein said at least one polymorphic simple sequence repeat locus is in a non-coding region of said genome.

3. The method of claim 1, wherein said prokaryote is of the genus *Escherichia*.

4. The method of claim 3, wherein said prokaryote is *Escherichia coli*.

5. The method of claim 1, wherein said prokaryote is of a genus selected from the group consisting of *Aquifex, Treponema, Bacillus, Listeria* and *Mycobacterium*.

6. The method of claim 5, wherein said prokaryote is selected from the group consisting of *Aquifex aeolicus, Treponema pallidum, Bacillus subtilis, Listeria monocytogenes* and *Mycobacterium tuberculosis*.

7. The method of claim 1, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilius, Mycoplasma, Helicobacter, Methanococcus, Archaeoglobus* and *Synechocystis*.

8. The method of claim 7, wherein said prokaryote is selected from the group consisting of *Haemophilius influenzae, Mycoplasma pneumoniae, Helicobacter pylori, Methanococcus jannaschii, Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

9. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by an allele specific oligonucleotide hybridization.

Independent

10. The method of claim 9, wherein said allele specific oligonucleotide hybridization is effected over a surface of DNA chip.

11. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by a polymerase chain reaction.

12. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by a sequencing reaction.

13. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by a heteroduplex hybridization reaction.

14. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by single strand conformational polymorphism.

15. The method of claim 1, wherein characterizing said at least one polymorphic simple sequence repeat locus in said genome of said prokaryote is effected by restriction fragment length polymorphism.

16. A pair of polymerase chain reaction primers having a sequence adapted for exponential amplification of a polymorphic simple sequence repeat locus in a genome of a prokaryote.

17. A polymerase chain reaction product derived by amplifying a portion of said genome using the pair of polymerase chain reaction primers of claim 16.

18. The pair of polymerase chain reaction primers of claim 16, wherein said polymorphic simple sequence locus is in a non-coding region of said genome.

19. The pair of polymerase chain reaction primers of claim 16, wherein said prokaryote is of the genus *Escherichia*.

20. The pair of polymerase chain reaction primers of claim 19, wherein said prokaryote is *Escherichia coli*.

21. The pair of polymerase chain reaction primers of claim 16, wherein said prokaryote is of a genus selected from the group consisting of *Aquifex, Treponema, Bacillus, Listeria* and *Mycobacterium*.

22. The pair of polymerase chain reaction primers of claim 21, wherein said prokaryote is selected from the group consisting of *Aquifex aeolicus, Treponema pallidum, Bacillus subtilis, Listeria monocytogenes* and *Mycobacterium tuberculosis*.

23. The pair of polymerase chain reaction primers of claim 16, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilus, Mycoplasma, Helicobacter, Methanococcus, Archaeoglobus* and *Synechocystis*.

24. The pair of polymerase chain reaction primers of claim 23, wherein said prokaryote is selected from the group consisting of *Haemophilus influenzae, Mycoplasma pneumoniae, Helicobacter pylori, Methanococcus jannaschii, Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

25. An allele specific oligonucleotide comprising a sequence of nucleotides adapted for effectively hybridizing only with a specific simple sequence repeat of a polymorphic simple sequence repeat locus in a genome of a prokaryote, under stringent allele specific oligonucleotide hybridization conditions of (i) a hibridization solution of 2 x standard sodium citrate (SSC) and 0.1 % sodium dodecyl sulfate (SDS); (ii) a hybridization temperature of from 42 °C to Tm - 5 °C for 30 minutes to overnight, wherein Tm is estimated as 2 x (the number of A plus T residues) + 4 x (the number of G plus C residues); and (iii) post hybridization washes with 0.75 x SSC and 0.1 % SDS at a temperature from 42 °C to Tm - 5 °C.

26. The allele specific oligonucleotide of claim 25, wherein said sequence of nucleotides is perfectly complementary to said specific simple sequence repeat.

27. A hybrid of the allele specific oligonucleotide of claim 25 and said specific simple sequence repeat.

28. The allele specific oligonucleotide of claim 25, wherein said polymorphic simple sequence locus is in a non-coding region of said genome.

29. The allele specific oligonucleotide of claim 25, wherein said prokaryote is of the genus *Escherichia*.

30. The allele specific oligonucleotide of claim 29, wherein said prokaryote is *Escherichia coli*.

31. The allele specific oligonucleotide of claim 25, wherein said prokaryote is of a genus selected from the group consisting of *Aquifex, Treponema, Bacillus, Listeria* and *Mycobacterium*.

32. The allele specific oligonucleotide of claim 31, wherein said prokaryote is selected from the group consisting of *Aquifex aeolicus,*

Treponema pallidum, Bacillus subtilis, Listeria monocytogenes and *Mycobacterium tuberculosis*.

33. The allele specific oligonucleotide of claim 25, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilius, Mycoplasma, Helicobacter, Methanococcus, Archaeoglobus* and *Synechocystis*.

34. The allele specific oligonucleotide of claim 33, wherein said prokaryote is selected from the group consisting of *Haemophilius influenzae, Mycoplasma pneumoniae, Helicobacter pylori, Methanococcus jannaschii, Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

35. A primer having a sequence adapted for amplification of a polymorphic simple sequence repeat locus in a genome of a prokaryote.

36. The primer of claim 35, wherein said polymorphic simple sequence locus is in a non-coding region of said genome.

37. The primer of claim 35, wherein said prokaryote is of the genus *Escherichia*.

38. The primer of claim 37, wherein said prokaryote is *Escherichia coli*.

39. The primer of claim 35, wherein said prokaryote is of a genus selected from the group consisting of *Aquifex, Treponema, Bacillus, Listeria* and *Mycobacterium*.

40. The primer of claim 39, wherein said prokaryote is selected from the group consisting of *Aquifex aeolicus, Treponema pallidum, Bacillus subtilis, Listeria monocytogenes* and *Mycobacterium tuberculosis*.

41. The primer of claim 35, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilius, Mycoplasma, Helicobacter, Methanococcus, Archaeoglobus* and *Synechocystis*.

42. The primer of claim 41, wherein said prokaryote is selected from the group consisting of *Haemophilius influenzae, Mycoplasma pneumoniae, Helicobacter pylori, Methanococcus jannaschii, Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

43. A DNA chip comprising a surface and a plurality of allele specific oligonucleotides attached thereto, each of said plurality of allele specific oligonucleotides including a sequence of nucleotides adapted for

effectively hybridizing only with a specific simple sequence repeat of a polymorphic simple sequence repeat locus in a genome of a prokaryote, under stringent allele specific oligonucleotide hybridization conditions of (i) a hibridization solution of 2 x standard sodium citrate (SSC) and 0.1 % sodium dodecyl sulfate (SDS); (ii) a hybridization temperature of from 42 ° C to Tm - 5 °C for 30 minutes to overnight, wherein Tm is estimated as 2 x (the number of A plus T residues) + 4 x (the number of G plus C residues); and (iii) post hybridization washes with 0.75 x SSC and 0.1 % SDS at a temperature from 42 °C to Tm - 5 °C.

44. The DNA chip of claim 43, wherein said sequence of nucleotides is perfectly complementary to said specific simple sequence repeat.

45. The DNA chip of claim 43, wherein said polymorphic simple sequence locus is in a non-coding region of said genome.

46. The DNA chip of claim 43, wherein said prokaryote is of the genus *Escherichia*.

47. The DNA chip of claim 46, wherein said prokaryote is *Escherichia coli*.

48. The DNA chip of claim 43, wherein said prokaryote is of a genus selected from the group consisting of *Aquifex, Treponema, Bacillus, Listeria* and *Mycobacterium*.

49. The DNA chip of claim 48, wherein said prokaryote is selected from the group consisting of *Aquifex aeolicus, Treponema pallidum, Bacillus subtilis, Listeria monocytogenes* and *Mycobacterium tuberculosis*.

50. The DNA chip of claim 43, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilius, Mycoplasma, Helicobacter, Methanococcus, Archaeoglobus* and *Synechocystis*.

51. The DNA chip of claim 50, wherein said prokaryote is selected from the group consisting of *Haemophilius influenzae, Mycoplasma pneumoniae, Helicobacter pylori, Methanococcus jannaschii, Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.